

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/576,496  
Source: FWP  
Date Processed by STIC: 5/1/06

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 05/01/2006

PATENT APPLICATION: US/10/576,496

TIME: 11:00:04

Input Set : A:\Q24468 Sequence Listing.txt

Output Set: N:\CRF4\05012006\J576496.raw

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3 <110> APPLICANT: Teijin Pharma Limited
4     Komori, Toshihisa
5     Kanatani, Naoko
6     Yoshida, Carolina Andrea
7     Zanma, Akira
8     Kobayashi, Shinji
9     Yamana, Kei
11 <120> TITLE OF INVENTION: BONE AND/OR JOINT-DISEASE-ASSOCIATES GENES
13 <130> FILE REFERENCE: Q94468
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/576,496
C--> 15 <141> CURRENT FILING DATE: 2006-04-20
15 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/015879
16 <151> PRIOR FILING DATE: 2004-10-20
18 <150> PRIOR APPLICATION NUMBER: JP 2003-359172
19 <151> PRIOR FILING DATE: 2003-10-20
21 <160> NUMBER OF SEQ ID NOS: 114
23 <170> SOFTWARE: PatentIn version 3.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 5220
27 <212> TYPE: DNA
28 <213> ORGANISM: Mouse
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (274)..(1962)
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38 ccggcagctc cacacagcag aacgccctgg gtccttgaaa ctcgaaaccc gggctcagaa      120
40 ccagcggaac ccaaagcgaa atccttgaac ttctctgaac aattgcttcc gggcgtttgc      180
42 tgagagccgg gggacctgac cggagcccag gccgcgtatg gcgcgcccct gatgtcacac      240
44 ggacgccagc gaggccagcg ctccggctgc agc atg gac cgc gcg ggc cgc ctg      294
45                                     Met Asp Arg Ala Gly Arg Leu
46                                     1               5
48 ggt gcg ggc ctg cgg gga ctc tgc gtg gct gca ctc gtg ctc gtg tgc      342
49 Gly Ala Gly Leu Arg Gly Leu Cys Val Ala Ala Leu Val Leu Val Cys
50      10               15               20
52 gcc gga cac ggg ggc cgc cgc gag gat ggg gga cca gct tgc tac gga      390
53 Ala Gly His Gly Gly Arg Arg Glu Asp Gly Gly Pro Ala Cys Tyr Gly
54      25               30               35
56 gga ttc gac ctc tac ttc atc ctg gac aag tca gga agt gtg ctg cac      438
57 Gly Phe Asp Leu Tyr Phe Ile Leu Asp Lys Ser Gly Ser Val Leu His
58 40               45               50               55
60 cac tgg aat gaa atc tac tac ttc gtg gag cag ttg gct cat aga ttc      486
61 His Trp Asn Glu Ile Tyr Tyr Phe Val Glu Gln Leu Ala His Arg Phe

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65	Ile Ser Pro Gln Leu Arg Met Ser Phe Ile Val Phe Ser Thr Arg Gly							
66		75		80		85		
68	aca act tta atg aaa cta act gag gac agg gaa cag atc cga caa ggc							582
69	Thr Thr Leu Met Lys Leu Thr Glu Asp Arg Glu Gln Ile Arg Gln Gly							
70		90		95		100		
72	cta gaa gag ctc cag aaa gtt ctg cca gga gga gac act tac atg cac							630
73	Leu Glu Glu Leu Gln Lys Val Leu Pro Gly Gly Asp Thr Tyr Met His							
74		105		110		115		
76	gaa gga ttc gag agg gcc agt gag cag att tac tat gag aac agt caa							678
77	Glu Gly Phe Glu Arg Ala Ser Glu Gln Ile Tyr Tyr Glu Asn Ser Gln							
78	120		125		130		135	
80	gga tac agg acg gcg agc gtc atc atc gcg ttg acg gat ggg gag ctg							726
81	Gly Tyr Arg Thr Ala Ser Val Ile Ile Ala Leu Thr Asp Gly Glu Leu							
82		140		145		150		
84	cac gag gac ctc ttc ttc tac tca gag agg gag gct aac cga tcc cga							774
85	His Glu Asp Leu Phe Phe Tyr Ser Glu Arg Glu Ala Asn Arg Ser Arg							
86		155		160		165		
88	gac ctt ggt gcg att gtt tac tgc gtt ggc gtg aag gat ttc aat gaa							822
89	Asp Leu Gly Ala Ile Val Tyr Cys Val Gly Val Lys Asp Phe Asn Glu							
90		170		175		180		
92	act cag ttg gct cgg att gca gac agt aag gac cac gtg ttt cct gtg							870
93	Thr Gln Leu Ala Arg Ile Ala Asp Ser Lys Asp His Val Phe Pro Val							
94		185		190		195		
96	aac gac ggc ttc cag gct ctc caa ggc att atc cac tca att tta aag							918
97	Asn Asp Gly Phe Gln Ala Leu Gln Gly Ile Ile His Ser Ile Leu Lys							
98	200		205		210		215	
100	aaa tcc tgc atc gaa att ctg gcg gct gaa cca tcc acc atc tgc gcg							966
101	Lys Ser Cys Ile Glu Ile Leu Ala Ala Glu Pro Ser Thr Ile Cys Ala							
102		220		225		230		
104	gga gag tcc ttt caa gtg gtc gta aga gga aat ggc ttc cga cat gcc							1014
105	Gly Glu Ser Phe Gln Val Val Val Arg Gly Asn Gly Phe Arg His Ala							
106		235		240		245		
108	cgc aat gtg gac agg gtc ctc tgc agc ttc aaa atc aat gac tca gtc							1062
109	Arg Asn Val Asp Arg Val Leu Cys Ser Phe Lys Ile Asn Asp Ser Val							
110		250		255		260		
112	acg ctc aat gag aag ccc ttt gct gtg gaa gac act tat ttg ctg tgc							1110
113	Thr Leu Asn Glu Lys Pro Phe Ala Val Glu Asp Thr Tyr Leu Leu Cys							
114		265		270		275		
116	cca gca cca atc ttg aaa gaa gtt ggc atg aaa gct gca ctg cag gtc							1158
117	Pro Ala Pro Ile Leu Lys Glu Val Gly Met Lys Ala Ala Leu Gln Val							
118	280		285		290		295	
120	agc atg aac gac ggc ctg tcc ttc atc tcc agt tct gtc atc atc acc							1206
121	Ser Met Asn Asp Gly Leu Ser Phe Ile Ser Ser Ser Val Ile Ile Thr							
122		300		305		310		
124	acc aca cac tgt tca gac ggc tcc atc ctg gcg att gct ctg ctg gtc							1254
125	Thr Thr His Cys Ser Asp Gly Ser Ile Leu Ala Ile Ala Leu Leu Val							
126		315		320		325		

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129	Leu	Phe	Leu	Leu	Leu	Ala	Leu	Ala	Leu	Leu	Trp	Trp	Phe	Trp	Pro	Leu	
130			330					335					340				
132	tgc	tgc	aca	gtg	atc	atc	aag	gag	gtc	cct	cca	ccc	cct	gtt	gag	gag	1350
133	Cys	Cys	Thr	Val	Ile	Ile	Lys	Glu	Val	Pro	Pro	Pro	Pro	Val	Glu	Glu	
134			345					350					355				
136	agt	gag	gaa	gaa	gaa	gat	gat	ggt	ttg	cca	aag	aag	aaa	tgg	ccc	aca	1398
137	Ser	Glu	Glu	Glu	Asp	Asp	Asp	Gly	Leu	Pro	Lys	Lys	Lys	Trp	Pro	Thr	
138	360							365					370			375	
140	gta	gat	gcc	tct	tat	tat	ggt	gga	cgc	ggt	gtg	gga	ggc	att	aaa	aga	1446
141	Val	Asp	Ala	Ser	Tyr	Tyr	Gly	Gly	Arg	Gly	Val	Gly	Gly	Ile	Lys	Arg	
142																390	
144	atg	gag	gtc	cgc	tgg	gga	gaa	aag	ggc	tcc	aca	gaa	gaa	ggg	gcg	aag	1494
145	Met	Glu	Val	Arg	Trp	Gly	Glu	Lys	Gly	Ser	Thr	Glu	Glu	Gly	Ala	Lys	
146																405	
148	tta	gaa	aag	gca	aag	aat	gca	cga	gtc	aag	atg	cca	gag	caa	gaa	tat	1542
149	Leu	Glu	Lys	Ala	Lys	Asn	Ala	Arg	Val	Lys	Met	Pro	Glu	Gln	Glu	Tyr	
150																420	
152	gag	ttc	cca	gaa	ccc	aga	aac	ctc	aac	aac	aac	atg	cgc	cgg	cct	tcc	1590
153	Glu	Phe	Pro	Glu	Pro	Arg	Asn	Leu	Asn	Asn	Asn	Met	Arg	Arg	Pro	Ser	
154																435	
156	tcg	cct	cgg	aag	tgg	tac	tcg	ccc	atc	aag	gga	aaa	ctc	gat	gcc	ttg	1638
157	Ser	Pro	Arg	Lys	Trp	Tyr	Ser	Pro	Ile	Lys	Gly	Lys	Leu	Asp	Ala	Leu	
158	440															455	
160	tgg	gtt	ctg	ctg	aga	aaa	gga	tat	gac	cga	gtg	tct	gtg	atg	agg	cca	1686
161	Trp	Val	Leu	Leu	Arg	Lys	Gly	Tyr	Asp	Arg	Val	Ser	Val	Met	Arg	Pro	
162																470	
164	cag	cca	gga	gac	acg	gga	cgc	tgt	atc	aac	ttc	acc	aga	gtg	aag	aac	1734
165	Gln	Pro	Gly	Asp	Thr	Gly	Arg	Cys	Ile	Asn	Phe	Thr	Arg	Val	Lys	Asn	
166																485	
168	agt	cag	cca	gcc	aag	tat	ccc	ctg	aac	aac	acc	tac	cac	ccc	agc	tcc	1782
169	Ser	Gln	Pro	Ala	Lys	Tyr	Pro	Leu	Asn	Asn	Thr	Tyr	His	Pro	Ser	Ser	
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172	cca	cct	ccc	gct	cct	atc	tac	aca	ccc	cca	ccc	cct	gct	ccc	cac	tgc	1830
173	Pro	Pro	Pro	Ala	Pro	Ile	Tyr	Thr	Pro	Pro	Pro	Pro	Ala	Pro	His	Cys	
174																515	
176	cct	ccc	cca	gcc	ccc	agt	gcc	ccc	act	cct	ccc	att	cct	tcc	cca	cca	1878
177	Pro	Pro	Pro	Ala	Pro	Ser	Ala	Pro	Thr	Pro	Pro	Ile	Pro	Ser	Pro	Pro	
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180	tcc	act	ctc	ccc	cct	cct	cct	cag	gcc	cca	ccc	cct	aac	agg	gca	cct	1926
181	Ser	Thr	Leu	Pro	Pro	Pro	Pro	Gln	Ala	Pro	Pro	Pro	Asn	Arg	Ala	Pro	
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184	ccc	ccc	tcc	cga	cct	cct	cca	agg	cct	tct	gtc	tag	aacccaaagt				1972
185	Pro	Pro	Ser	Arg	Pro	Pro	Pro	Arg	Pro	Ser	Val						
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188	ccgagctctg	ggctgctga	gcaactccag	caggaggctt	ctctgctgaa	agaaagatct											2032
190	gcccagccta	tgtggtgagt	ggcggctgat	gtttgcacga	tttaaaagca	agtcgtgatg											2092
192	ggcagaacaa	aatgggcatt	ttgaactgcc	tgaagacaga	caatgagaca	ataacagtca											2152
194	cattatagcc	tgtgaccctt	cacctctaga	ggaagggttc	cgagatggcc	acattgccac											2212

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202	gtgcagtgtc	cctagtatgc	atcgaatagg	tatccaactg	ggatctgcag	gttgcccttat	2452
204	aaagagcata	tgtctctatc	tctttcccga	acttcctggg	ttcccagtga	tgagggaagg	2512
206	ggaaaggtgt	tgccatgctt	agaagttaga	ggacgtcagt	gctcagcact	gatggagaag	2572
208	cgttgatggg	agtgtccagc	tcttacatct	agaaatgggt	gggttcagca	ggcacagtct	2632
210	ctaaaccaac	aagccttgct	attgtcaaag	gcaacctact	aatgattcac	cttaaacatc	2692
212	aaggttgact	gtggcatagg	tcagagctga	tcacacagaa	ccttccccat	gaaatcgcaa	2752
214	ggttcctcat	cttcaaatac	ccaggacccc	agagatttct	aaatccagct	aagagacagt	2812
216	agtcctgact	tggcaagaaa	accattccca	gttgttttac	tctgaaacag	gccgttgtat	2872
218	gtatggtata	tctctccttg	gcctttcaac	ctgtctcaca	gtattaccag	ttatgaagca	2932
220	aggagaaata	catccagtgt	gtaatagaaa	agctctgccc	acaatcccca	tgtcactcct	2992
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264	aacaggagat	ggtggttggt	attagcaaac	tgcatgtgtt	atttgtttga	ctccttgtta	4312
266	ttgtccttac	ggaggatttt	ttttatataa	gccaaatttt	gttgatatata	ttcatattcc	4372
268	acgtgacaga	tggaagcacg	tcctatcagt	gtgaataaaa	agaacagttg	tagtaaatta	4432
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282	tgatggtgga	aaatccatca	aggaataatt	gtgagataat	gaccgacagt	tcaggcgcaa	4852
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286	ttactcacca	ggaggatgga	aagggttttt	ttagttatct	gagctcagct	gagttatcac	4972
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290	tcttctcttt	ttctatggta	atttagttat	ggacgttcag	cgtctctgag	ttattgttat	5092
292	aaaagacttg	tcataccgcg	actgtgctgt	aggagactgg	gctgaacctg	tacaatggta	5152

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301 <212> TYPE: PRT
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311 20 25 30
314 Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile Leu Asp
315 35 40 45
318 Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr Phe Val
319 50 55 60
322 Glu Gln Leu Ala His Arg Phe Ile Ser Pro Gln Leu Arg Met Ser Phe
323 65 70 75 80
326 Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr Glu Asp
327 85 90 95
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331 100 105 110
334 Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser Glu Gln
335 115 120 125
338 Ile Tyr Tyr Glu Asn Ser Gln Gly Tyr Arg Thr Ala Ser Val Ile Ile
339 130 135 140
342 Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr Ser Glu
343 145 150 155 160
346 Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr Cys Val
347 165 170 175
350 Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala Asp Ser
351 180 185 190
354 Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu Gln Gly
355 195 200 205
358 Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu Ala Ala
359 210 215 220
362 Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val Val Arg
363 225 230 235 240
366 Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu Cys Ser
367 245 250 255
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371 260 265 270
374 Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu Val Gly
375 275 280 285
378 Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser Phe Ile
379 290 295 300
382 Ser Ser Ser Val Ile Ile Thr Thr Thr His Cys Ser Asp Gly Ser Ile
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386 Leu Ala Ile Ala Leu Leu Val Leu Phe Leu Leu Leu Ala Leu Ala Leu
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**VERIFICATION SUMMARY**

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Input Set : A:\Q94468 Sequence Listing.txt

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L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date